Raw Sequence Listing Error Summary

ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 09/763,978

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

11 _____ Use of "Artificial" (NEW RULES)
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

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                    PATENT APPLICATION:  US/09/763,978   TIME: 13:29:15

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C--> 2 <141> CURRENT FILING DATE: 2001-02-28
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W--> 0 <110> APPLICANT:
W--> 0 <120> TITLE INVENTION:
W--> 0 <130> FILE REFERENCE:

Does Not Comply Corrected Diskette Needed

see p. 6 for explanation

see pp 5, 6

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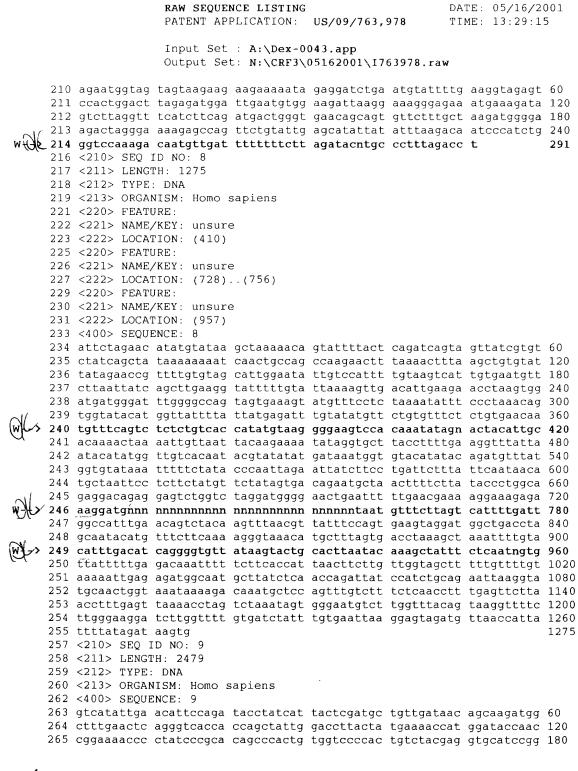
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258 <211> LENGTH: 2479
259 <212> TYPE: DNA
260 <213> ORGANISM: Homo sapiens
262 <400> SEQUENCE: 9
263 gtcatattga acattccaga tacctatcat tactcgatgc tgttgataac agcaagatgg 60
264 ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaaccat ggataccaac 120
265 cggaaaaccc ctatcccgca cagcccactg tggtccccac tgtctacgag gtgcatccgg 180
```

Please Note:
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.**

Insert these *manda* numeric identifiers *and responses* *delete this*

~~SEQUENCE LISTING~~

☐
<151> 1998-09-02
☐

☐
<160> 15
☐

☐
<170> PatentIn Ver. 2.0

see item 13 on Error Summary sheet

<1107>
<1207>
<1407>
<1417>
<1507>

Input Set : **A:\Dex-0043.app**
Output Set: **N:\CRF3\05162001\I763978.raw**

```
L:2 M:270 C: Current Application Number differs, Replaced Current Application No
L:2 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2 M:289 W: Identifier Missing or Out-Of-Order, <150> PRIOR APP NO
L:0 M:201 W: Mandatory field data missing, APPLICANT NAME
L:0 M:201 W: Mandatory field data missing, TITLE INVENTION
L:0 M:201 W: Mandatory field data missing, FILE REFERENCE
L:176 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:214 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:240 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:246 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:249 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:363 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
L:363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:367 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
L:367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:369 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
L:369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
```